

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on 16.Jan.2003, 16:19:12, Search time: 20.4 Seconds
(without alignments)

28,464 Million cell updates/sec

Title: US-09-856-070-17

perfect score: 69

Sequence: 1 EREKOMMRFKEEL 14

Scoring table: BL05062

Gapop 10.0 , Gapext. 0.5

Searched: 112892 seqs, 4;476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 6

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40;*

Score: 8

Quality: 9

Match: 100.0

Length: 14

DB ID:

SUMMARIES

Result No.: 1

Score: 69

Length: 100.0

DB ID: P31976

Description: bos taurus

EZR_BOVIN

Score: 69

Length: 100.0

DB ID: P31976

Description: hom sapien

EZR_HUMAN

Score: 66

Length: 95.7

DB ID: P31976

Description: mus musculus

EZR_MOUSE

Score: 66

Length: 95.7

DB ID: P31976

Description: rhesus

EZR_MACACA

Score: 66

Length: 95.7

DB ID: P31976

Description: hom sapien

EZR_HUMAN

Score: 66

Length: 95.7

DB ID: P31976

Description: bovis

EZR_BVIRUS

Score: 66

Length: 95.7

DB ID: P31976

Description: canis lupus familiaris

EZR_CANIS

Score: 66

Length: 95.7

DB ID: P31976

Description: equus caballus

EZR_EQUIUS

Score: 66

Length: 95.7

DB ID: P31976

Description: sus scrofa

EZR_PIG

Score: 66

Length: 95.7

DB ID: P31976

Description: ovis aries

EZR_OVIS

Score: 66

Length: 95.7

DB ID: P31976

Description: spodoptera frugiperda

EZR_SPIDER

Score: 66

Length: 95.7

DB ID: P31976

Description: arthropoda

EZR_ARACHNID

Score: 66

Length: 95.7

DB ID: P31976

Description: rana temporaria

EZR_FROG

Score: 66

Length: 95.7

DB ID: P31976

Description: rana esculenta

EZR_FROG

Score: 66

Length: 95.7

DB ID: P31976

Description: rana temporaria

EZR_FROG

Score: 66

Length: 95.7

DB ID: P31976

Description: rana temporaria

EZR_FROG

Score: 66

Length: 95.7

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Description: rana temporaria

EZR_FROG

Score: 66

Length: 95.7

DB ID: P31976

Description: rana temporaria

EZR_FROG

Score: 66

Length: 95.7

DB ID: P31976

Description: rana temporaria

CC TISSUE SPECIFICITY: COMPONENT OF THE MICROVILLI OF INTESTINAL EPITHELIAL CELLS.
 CC PTM - PHOSPHYLATED BY PROTEIN-TYROSINE KINASES.

CC -!- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.

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CC IDENTIFIERS: EMBL: X60671; CAA43086; 1; -.

DR PIR: BA1129; B41129.

DR MGI: 98931; Vill2.

DR InterPro: IPR000299; Band_4_1.

DR InterPro: IPR000798; Ezr/rad/moesin.

DR Pfam: PF00373; Band_4_1; 1.

DR PRINTS: PRO0935; BAND41.

DR SMART: SM0024K; R41_1.

DR PROSITE: PS00660; BAND_41_1; 1.

DR PROSITE: PS00661; BAND_41_2; 1.

DR PROSITE: PS50057; BAND_41_3; 1.

KW Structural protein; Cytoskeleton; Phosphorylation.

FT INIT_MET 0 BY SIMILARITY.

FT DOMAIN 0 224 BAND 4.1-LIKE.

FT MOD_RES 145 145 PHOSPHORYLATION (BY PDGF)

FT MOD_RES 353 353 (BY SIMILARITY).

FT PHOSPHORYLATION (BY PDGFR)

FT PHOSPHORYLATION (BY SIMILARITY).

SQ SEQUENCE 585 AA, 69214 MW, (2072EDE2B03532 CRC64,

Query Match 95.78; Score 66; DB 1; Length 585;
 Best Local Similarity 92.98; Pred. No. 0.036;
 Matches 13, Conservative 1; Mismatches 0; Gaps 0;

QY 1 EREKOMREREKEEL 14

Db 333 EREKOMREREKEEL 346

RESULT 4

MOES_MOUSE STANDARD; PRT; 576 AA.

ID MOES_MOUSE STANDARD; PRT; 576 AA.

AC P26041; AC P26041; DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DE Moesin (Membrane-organizing extension spike protein),
 GN Mus musculus (Mouse).
 OC Eukaryota; Chordata; Crustacea; Vertebrata; Euteleostomi;
 RA Trifolia S.; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OM NCBI_TAXID:10650; RN [1] SEQUENCE FROM N.A., AND SEQUENCE OF 1-15; 54-59 AND 413-434
 OC TISSUE_Placenta; Mammalia; Eutheria; Primates; Cetartiodactyla; Homo.
 OX NCBI_TAXID:9606; RA Lankes W.T., Furthmayr H.,
 RN [1] "Moesin", a member of the protein 4.1-talin-intinin family of proteins.";
 RP PROTEIN_NAIL_Acid_Seq_HUMAN_AR.R297-A91(9q1) PX SHEDDING_OF_11-57b FROM N.A.
 RN [2] SEQUENCE FROM N.A. PX MEDLINE:924374; PubMed:1573844;
 RA Hoden P.; RA Furthmayr H., Lankes W.T., Anieva M.R.,
 RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. RT ROLE IN CELLULAR FUNCTIONS.
 RX MEDLINE:92220940; PubMed:19243894; KL Kidney Int 41:665-670(1992).
 CC -!- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETON. CC STRUCTURES TO THE PLASMA MEMBRANE.
 CC -!- TISSUE SPECIFICITY: IN ALL TISSUES AND CULTURED CELLS STUDIED.
 CC -!- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
 CC -!- DATABASE: NAME=Atlas Genet Cytogenet Oncol Haematol
 CC WWW=<http://www.infobiofgen.fr/services/chromocancer/Genes/MSN1163.html>

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CC EMBL: M70495; AAAV3IC; 1; -.

DR PIR: A41289; A11289.

DR Parhus/Ghent-2DPAGE: 3515; IEF.

DR Parhus/Ghent-2DPAGE: 3516; IEF.

DR Genew, ISGN: 7373, MSN.

DR MIM: 309845; DR InterPro: IPE000299; Band_4_1.

DR InterPro: IPR000798; Ezr/rad/moesin.

DR Pfam: PF00373; Band_4_1; 1.

DR PRINTS: PRO0935; BAND41.

DR SWAP: SM00295; B41_1.

DR PROSITE: PS00660; BAND_41_1; 1.

DR PROSITE: PS00661; BAND_41_2; 1.

DR PROSITE: PS50057; BAND_41_3; 1.

KW Structural protein; Cytoskeleton.

FT INIT_MET 0 BY SIMILARITY.

FT DOMAIN 57 224 BAND 4.1-LIKE.

SQ SEQUENCE 576 AA: 67684 MW, 9477628D5A8176 CRC64;

Query Match 73.9%; Score 51; DB 1; Length 576;
 Best Local Similarity 71.4%; Pred. No. 3.9%;
 Matches 16; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

RESULT 5

MOES_MOUSE STANDARD; PRT; 576 AA.

ID MOES_MOUSE STANDARD; PRT; 576 AA.

AC P26041; AC P26041; DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)

DE Moesin (Membrane-organizing extension spike protein),
 GN Mus musculus (Mouse).
 OC Eukaryota; Chordata; Crustacea; Vertebrata; Euteleostomi;
 RA Trifolia S.; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OM NCBI_TAXID:10650; RN [1] SEQUENCE FROM N.A., AND SEQUENCE OF 1-15; 54-59 AND 413-434
 OC TISSUE_Placenta; Mammalia; Eutheria; Primates; Cetartiodactyla; Homo.
 OX NCBI_TAXID:9606; RA Lankes W.T., Furthmayr H.,
 RN [1] "Moesin", a member of the protein 4.1-talin-intinin family of proteins.";
 RP PROTEIN_NAIL_Acid_Seq_HUMAN_AR.R297-A91(9q1) PX SHEDDING_OF_11-57b FROM N.A.
 RN [2] SEQUENCE FROM N.A. PX MEDLINE:924374; PubMed:1573844;
 RA Hoden P.; RA Furthmayr H., Lankes W.T., Anieva M.R.,
 RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. RT ROLE IN CELLULAR FUNCTIONS.
 RX MEDLINE:92220940; PubMed:19243894; KL Kidney Int 41:665-670(1992).
 CC -!- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETON. CC STRUCTURES TO THE PLASMA MEMBRANE.
 CC -!- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
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CC	DR	SMART; SM00295; B41; 1.
CC	DR	PROSITE; PS00660; BAND_41_1; 1.
CC	DR	PROSITE; PS00661; BAND_41_2; 1.
CC	DR	PROSITE; PS50057; BAND_41_3; 1.
CC	KW	structural protein; cytoskeleton.
CC	FT	INIT_MET 0
CC	FT	DOMAIN 0
CC	FT	DOMAIN 57 224
CC	SQ	SEQUENCE 576 AA; 67529 MW; 3CE0B7/8E5F75E6B CRC64;
DR	DR	INTERPRO; IPI00299; Band_4_1.
DR	DR	PROSITE; IPI00798; Ez/rad/mosin.
DR	DR	PTM; PF00373; Band_41; 1.
DR	DR	PTM; PF00769; ERM; 1.
DR	PRINTER; PR00935; BAND41.	
DR	PRINTER; SM00295; B41; 1.	
DR	PROSITE; PS00660; BAND_41_1; 1.	
DR	PROSITE; PS00661; BAND_41_2; 1.	
DR	PROSITE; PS50057; BAND_41_3; 1.	
CC	KW	structural protein; cytoskeleton.
CC	FT	INIT_MET 0
CC	FT	DOMAIN 57 224
CC	FT	DOMAIN 576 AA; 67529 MW; 3CE0B7/8E5F75E6B CRC64;
DR	DR	INTERPRO; IPI00299; Band_4_1.
DR	DR	PROSITE; IPI00798; Ez/rad/mosin.
DR	DR	PTM; PF00373; Band_41; 1.
DR	DR	PTM; PF00769; ERM; 1.
DR	PRINTER; PR00935; BAND41.	
DR	PRINTER; SM00295; B41; 1.	
DR	PROSITE; PS00660; BAND_41_1; 1.	
DR	PROSITE; PS00661; BAND_41_2; 1.	
DR	PROSITE; PS50057; BAND_41_3; 1.	
CC	KW	BY SIMILARITY
CC	FT	DOMAIN 4_1-LIKE.
CC	SQ	SEQUENCE 576 AA; 67529 MW; 3CE0B7/8E5F75E6B CRC64;
DR	DR	Query Match 73.9%; Score 51; DB 1; length 576;
DR	DR	Best Local Similarity 71.4%; Pred. No. 3..9;
DR	DR	Matches 10; conservative 3; Mismatches 1; Indels 0; Gaps 0;
DR	DR	Qy 1 EREKEMMREKEEL 14
DR	DR	Db 333 EKEEKERKEEL 346
DR	DR	RESULT 7
DR	DR	RAD1_HUMAN STANDARD; PRT: 583 AA.
DR	DR	ID RAD1_HUMAN STANDARD; PRT: 583 AA.
DR	DR	AC P35241;
DR	DR	BI 01-FEB-1994 (Rel. 28, Created)
DR	DR	BT 01-FEB-1994 (Rel. 28, Last sequence update)
DR	DR	DT 16-OCT-2001 (Rel. 40, Last annotation update)
DR	DR	DE Radixin.
DR	DR	GN
DR	DR	OS Homo sapiens (Human).
DR	DR	EC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DR	DR	OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
DR	DR	NCBI_TaxID:9006; RN [1]
DR	DR	SEQUENCE FROM N.A.
DR	DR	TISSUE-LIVER
DR	DR	RX MEDLINE-93252378; PubMed-8486357;
DR	DR	RA Wiltgenbus K.K., Miatro维奇 A., Francke U., Furtmayr H.;
DR	DR	"Molecular cloning, cDNA sequence, and chromosomal assignment of the human radixin gene and two dispersed pseudogenes."
DR	DR	RL Genomics 16:199-206(1993).
CC	CC	-1- FUNCTION probably plays a crucial role in the binding of the barbed end of actin filaments to the plasma membrane.
CC	CC	-1- SUBCELLULAR LOCALIZATION: HIGHLY CONCENTRATED IN THE UNDERCOAT OF THE CELL-TO-CELL ADHERENS JUNCTION AND THE CLEAVAGE FURROW IN THE INTERPHASE AND MITOTIC PHASE, RESPECTIVELY
CC	CC	-1- SIMILARITY: CONTAINS 1 HAND 4_1-LIKE DOMAIN.
CC	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	CC	EMBL; L023320; AAA36541; 1;
CC	CC	PTR; A46127; A46127.
CC	CC	BR Arthrop.Chant 20:PAGE; 25/01; IEP.
CC	CC	DR Genow; HCNC:9944; RDX.
CC	CC	MIM: 173410; -;
CC	CC	InterPro; IPI000239; Band_4_1.
CC	CC	InterPro; IPI000798; Ez/rad/moesin.
CC	CC	Ptmt; PF00373; Band_4_1.
CC	CC	Ptmt; PF00769; ERM; 1.
CC	CC	PRINUS; PR00935; BAND41.
CC	CC	SMART; SM00295; B41; 1.
CC	CC	DR PROSITE; PS00660; BAND_41_1; 1.
CC	CC	DR PROSITE; PS00661; BAND_41_2; 1.
CC	CC	DR PROSITE; PS50057; BAND_41_3; 1.
CC	CC	KW structural protein; cytoskeleton; Actin-binding; Capping protein.
CC	CC	FT DOMAIN 58 225
CC	CC	FT DOMAIN 470 477
CC	CC	SQ SEQUENCE 583 AA; 68564 MW; 884967/E1D675FF7 CRC64;

Query Match 73.9%; Score 51; DB 1; Length 583;
Best local Similarity 71.4%; Pred. No. 4;
Matches 10; Conservative 3; M.matches 1; Indels 0; gaps 0;

QY 1 EREKEQMREKEEL 14
ID :|||:|||||
Db 334 EKEKEERKEEL 347

RESULT 8
RADI_MOUSE:
ID RADI_MOUSE; STANDARD; PRT; 583 AA.
AC P26043;
DI 01-MAY-1992 (Rel. 22, created)
DT 01-MAY-1992 (Rel. 22, last sequence update)
DE 16-OCT-2001 (Rel. 40, last annotation update)
RN 1
GN RADIXIN
OS Mus musculus (Mouse); Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; NCBI_TAXID=10090;
OX [1] SEQUENCE FROM N.A., AND SEQUENCE OF 28-53 AND 263-277.
PP TISSUE-liver;
EC MEDLINE:92054535; PubMed:1955155;
RA Furukawa N.; Nagatuchi A.; Saito N.; Tsukita S.; Tsukita S.;
RA F.;
RL J. Cell Biol. 115:1019-1048(1991).
CC -1- FUNCTION: PROBABLY PLAYS A CRUCIAL ROLE IN THE BINDING OF ACTIN FILAMENTS TO THE PLASMA MEMBRANE.
CC -1- SUBCELLULAR LOCATION: HIGHLY CONCENTRATED IN THE UNDERCOAT OF THE CELL-TO-CELL ADHERENS JUNCTION AND THE CLEAVAGE FURROW IN THE INTERPHASE AND MITOTIC PHASE, RESPECTIVELY.
CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
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CC EMBL: Xbase: AAA4 (rel. 1);
DR PIR: A41129; A41129;
DR MGDB: MGI:97887; PDX;
DR InterPro: IPR00299; Band_4.1;
DR Pfam: PF00373; Band_4.1;
DP PRINTS: PRO0935; BAND41.
DR SMART: SM00295; B41_1.
DR PROSITE: PS00660; BAND_4.1_1;
DR PROSITE: PS00661; BAND_4.1_2;
DR PROSITE: PS50057; BAND_4.1_3;
KW Structural protein; cytoskeleton; Actin-binding; Capping protein, FT DOMAIN 58 225 BAND 4.1-LIKE.
FT DOMAIN 470 477 POLY PRO.
SQ SEQUENCE 583 AA; 68451 MW; 3219A52RCDCB7EB; CRC64;

Query Match 73.9%; Score 51; DB 1; Length 583;
Best local Similarity 71.4%; Pred. No. 4;
Matches 10; Conservative 3; M.matches 1; Indels 0; gaps 0;

QY 1 EREKEQMREKEEL 14
ID :|||:|||||
Db 334 EKEKEERKEEL 347

RESULT 9
RADL_PIG:
ID RADL_PIG; STANDARD; PRT; 583 AA.

Medline:9-260018; PubMed:7684041;
Fietz M.J.; McLaughlin C.J.; Campbell M.T.; Rogers G.E.;
"Analysis of the sheep trichohyalin gene: potential structural and
calcium-binding roles of trichohyalin in the hair follicle.";
J. Cell Biol. 121:855-865(1993).
[2]
SEQUENCE OF 1016-1549 FROM N.A.
STRAN-MERINO HORSE HORN X BORDER LEISTER TISSUE-WOOL FOLLICLES;
Fietz M.J.; Presland R.B.; Rogers G.E.;
The cDNA deduced amino acid sequence for trichohyalin, a
differentiation marker in the hair follicle, contains a 23 amino acid
repeat:
J. Cell Biol. 110:427-436(1990)
SEQUENCE OF 1016-1549 FROM N.A.
STRAN-MERINO HORSE HORN X BORDER LEISTER TISSUE-WOOL FOLLICLES;
Fietz M.J.; Presland R.B.; Rogers G.E.;
"Analysis of the sheep trichohyalin gene: potential structural and
calcium-binding roles of trichohyalin in the hair follicle.";
J. Cell Biol. 121:855-865(1993).
[2]
SEQUENCE OF 1016-1549 FROM N.A.
STRAN-MERINO HORSE HORN X BORDER LEISTER TISSUE-WOOL FOLLICLES;
Fietz M.J.; Presland R.B.; Rogers G.E.;
The cDNA deduced amino acid sequence for trichohyalin, a
differentiation marker in the hair follicle, contains a 23 amino acid
repeat:
J. Cell Biol. 110:427-436(1990)
FUNCTION: INTERMEDIATE FILAMENT-ASSOCIATED PROTEIN THAT ASSOCIATES
IN REGULAR ARRAYS WITH KERATIN INTERMEDIATE FILAMENTS (KIF) OF THE
INNER ROOT SHEATH CELLS OF THE HAIR FOLLICLE AND THE SPANIEL
LAYER OF THE EPIDERMIS. IT LATER BECOMES CROSS-LINKED TO KIF BY
LISODIPEPTIDE BONDS. IT MAY SERVE AS SCAFFOLD PROTEIN, TOGETHER
WITH INVOLUCRIN, IN THE ORGANIZATION OF THE CPII-FNIV CODE OF EVEN
ANCHOR THE CELL ENVELOPE TO THE KIF NETWORK. IT MAY BE INVOLVED IN
ITS OWN CALCIUM-DEPENDENT POSTSYNTHETIC PROCESSING DURING TERMINAL
DIFFERENTIATION.
SUBUNIT: HOMODIMER (PROBABLE).
ALTERNATIVE PRODUCTS: AT LEAST TWO FORMS MAY BE PRODUCED BY
ALTERNATIVE SPLICING OF THE SAME GENE.
Tissue specificity: found in the hair keratinizing tissues such as
the inner root sheath (IRS) of hair follicles and medulla, and in
the epithelia of the tongue, hoof and rumen.
DOMAIN: CONSISTS OF NINE DOMAINS. DOMAIN 1 CONTAINS TWO EF-HAND
CALCIUM-BINDING DOMAINS 2-4, 6, AND 8 ARE ALMOST
ENTIALLY ALPHA-HELICAL, CONFIGURED AS A SERIES OF PEPTIDE REPEATS
OF VARYING REGULARITY, AND ARE THOUGHT TO FORM A SINGLE-STRETCHED
ALPHA-HELICAL ROD STABILIZED BY IONIC INTERACTIONS. DOMAIN 6 IS
THE MOST REGULAR AND MAY BIND KIF DIRECTLY BY IONIC INTERACTIONS.
DOMAINS 5 AND 7 ARE LESS WELL ORGANIZED AND MAY INDUCE FOLDS IN
THE MOLECULE. DOMAIN 9 CONTAINS THE C-TERMINUS, CONSERVED AMONG
DIFFERENT SPECIES.
PTM: SUBSTRATE OF TRANSGlutaminase SOME 200 ARGININES AND
PROBABLY CONVERTED TO CITRULLINES BY PEPTYDYLARGININE DEIMIDASE.
SIMILARITY: IN THE N TERMINAL SECTION: BELONGS TO THE S-100
FAMILY.
SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
EMBL: Z1B461; CAA79165.1;
EMBL: X51695; CAA5992.1;
EMBL: A34309; CAA5992.1;
PIR: S-2643; S-2639;
PIR: A40691; A40691;
HSSP: P02633; IIG5;
InterPro: IPR01751; CabP_S100;
InterPro: IPK002048; EF-hand;
IPK0036; CabP_S100;
IPK0023; S-100; 1;
Protein: P000407; CabP_S100; 1;
Prosite: PS00018; EF_HAND; 1;
Prosite: PS00403; S100_CABP; FALSE_NEG;
Keratinization: Repeat; Calcium-binding;
DOMAIN 1 91 S-100 like
CA_HIND 22 33 EF-HAND 1 (LOW AFFINITY) (POINT A);
CA_BIND 62 73 EF-HAND 2 (HIGH AFFINITY) (POINTIAL);
DOMAIN 413 832 14 X 28 AA APPROXIMATE TANDEM REPEATS.
REPEAT 413 448 1-1;
REPEAT 449 547 1-2;
REPEAT 477 504 1-3;

SEQUENCE FROM N.A. (ISOFORMS 1 TO 4).
 MEDLINE-2053946; PubMed-10447877.
 Berghs S., Aguirre D., Dirix P., Tr. Maksimova E., Stabach P., Ferreira T.M., Zhang J.-P., Philbrick W., Slepenev V., Ort T., Solimena M.

"Beta1 spectrin, a new spectrin localized at axon initial segments and nodes of ranvier in the central and peripheral nervous system." [3] Cell Biol 161:485-500 (2000).

SEQUENCE OF 386-2382 FPM_N_A (ISOFORM 1).
 TISSUE=Brain;
 ACRC
 MEDLINE-2144683; PubMed-10447877.
 Nagase T., Kuroki R., Nakayama M., Hirosewa M., Ohara O., XVII. The complete coding sequences of unidentified human genes. DNA Res. 7:273-281(2000).
 -1- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2, 3 and 4, are produced by alternative splicing.
 -1- TISSUE SPECIFICITY: Abundantly expressed in brain and pancreatic islets.

-1- SIMILARITY: CONTAINS 2 CALMODULIN (CaM) LIMAINS.
 -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
 -1- SIMILARITY: CONTAINS 18 SPECTRIN REPEATS.

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EMBL: AF082075; AAC38874; -;
 EMBL: AF082076; AAC38875; -;
 EMBL: AF082077; AAC38876; -;
 EMBL: AY004226; AAC93177; -;
 EMBL: AY004227; AAC93178; -;
 EMBL: AY004228; AAC93179; -;
 EMBL: AB046862; BAB13468; -;
 HSPP: Q01082; IBKR.
 ORF
 GeneID: HGNC-14896; SPINTH4
 NM_066214; -;
 InterPro: IPR001589; Actinbind_actinin.
 InterPro: IPR001715; Calponin-like.
 InterPro: IPR001849; PH.
 InterPro: IPR002017; Spectrin.
 InterPro: IPR001605; Spectrin_PH.
 Pfam: PF00169; PH; 3.
 Pfam: PE00307; CH; 2.
 Pfam: PF00435; spectrin; 56.
 PRINTS: PRO0081; SPECTRINPH.
 SMART: SM00033; CH; 2.
 SMART: SM00233; PH; 1.
 SMART: SM00150; SPIC; 16.
 PROSITE: PS00019; ACTIN_N-1; 1.
 PROSITE: PS00020; ACTIN_N-2; 1.
 PROSITE: PS50021; CH; 2.
 PROSITE: PS50003; PH_DOMAIN; 1.
 Cytoskeleton, Membrane, Repeat, Actin_binding, Capping protein, Alternative_splicing, DOMAIN [1] 282
 DOMAIN 6.1 165
 DOMAIN 18.0 282
 REPEAT 30.9 354
 REPEAT 39.8 419
 REPEAT 42.9 533
 REPEAT 5.35 642
 REPEAT 64.4 771
 REPEAT 77.3 879
 REPEAT 88.1 985
 REPEAT 101.9 1086
 REPEAT 108.8 1197
 ACTIN-BINDING (BY SIMILARITY).
 CH 1.
 CH 2.
 SPECTRIN 1.
 SPECTRIN 2.
 SPECTRIN 3.
 SPECTRIN 4.
 SPECTRIN 5.
 SPECTRIN 6.
 SPECTRIN 7.
 SPECTRIN 8.
 SPECTRIN 9.

F1	NON_TER	321	AA:	321	MW:	04844AD681F0714R C064;	
SD	SEQUENCE:	321					
Query Match	Best Local Similarity	62.3%	Score	43;	DB 1;	Length	321;
Matches B;	Conservative	61.5%	Pred No	27;	Indels	0;	Gaps 0;
QY	1 EREKSUMMREKEE 13						
DB	290 EKEKEKEKEKEKEE 302						
RESULT 13							
ABRA_PLAFC	ID: ABRA_PLAFC	STANDARD:	PFT:	743 AA.			
AC: P22629;	DT: 01-AUG-1991 (Rel. 19, created)						
DT: 15-JUL-1998 (Rel. 36, last sequence update)							
DE: 101 kDa malaria antigen (P101) (Acidic basic repeat antigen)							
GN: ABRA.							
OS: Plasmodium falciparum (isolate Camp / Malaysia)							
OC: Plasmodium falciparum (isolate Camp / Malaysia)							
OX: NCBI_TaxID:5835;							
RN: KP SEQUENCE FROM N.A.							
RX: MEDLINE-88298704; PubMed-3042768;							
RA: Weber J.-L., Lyon T. A., Wolitz B. H., Hall T., Lowell G. H., Chitay J. D.							
RT: "Primary structure of a Plasmodium falciparum malaria antigen located at the merozoite surface and the parasitophorous vacuole.";							
RU: Biol. Chem. 263:11421-11425 (1988).							
RC: SUBCELLULAR LOCATION: AT THE MEROZOITE SURFACE AND WITHIN THE PARASITOPIKOCUS VACUOLE.							
CC: -+; PRM: NOT GLYCOSYLATED (PROBABLE).							
CC: This SWISS-PROT entry is copyright.							
CC: It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation							
CC: the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions.							
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OR: EMBL; JO3902; AAA29462; 1;							
DR: PIR: A29232; A29232.							
KW: Antigen; Malaria; Repeat.							
FT: DOMAIN 226 273 REPEAT 226 231							
FT: REPEAT 232 237							
FT: REPEAT 238 243							
FT: REPEAT 244 249							
FT: REPEAT 250 255							
FT: REPEAT 256 261							
FT: REPEAT 262 267							
FT: REPEAT 268 273							
FT: DOMAIN 674 731							
SEQUENCE: 743 AA: 86622 MW: 4844AD681F0714R C064;							
Query Match	Best Local Similarity	62.3%	Score	43;	DB 1;	Length	743;
Matches B;	Conservative	61.5%	Pred No	62;	Indels	0;	Gaps 0;
QY	1 EREKSUMMREKEE 13						
DB	694 EKEKEKEKEKEKEE 706						
RESULT 14							
V182_HUMAN	ID: V182_HUMAN	STANDARD,	FRT,	1157 AA.			
AC: Q14687;							
DT: 01-NOV-1997 (Rel. 35, created)							
DT: 01-NOV-1997 (Rel. 35, last sequence update)							
RN: 13] SEQUENCE FOR 614-790 FROM N.A. (CENTROSOMIN A).							

RX MEDLINE-91277032; PubMed-1829085;
 RA Joswig G., Petzelt C., Werner D.;
 RT Murine cDNAs coding for the centrosomal antigen centrosomin A.
 RL J. cell sci. 98:37-43 (1991).
 RN [4].
 RP REVISIONS.
 RA Submitted (DEC 1996) to the EMBL/GenBank/CDD databases.
 RL -1- FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING OF
 CC -1- METIONYL-TRNAI AND MONA.
 CC -1- SUBUNIT: EIF-3 IS COMPOSED OF AT LEAST 10 DIFFERENT SUBUNITS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (By similarity).
 CC -1- PM: PHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE EIF3E10 FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 DR EMBL: U14172; AAQ90910; 1;
 DR EMBL: X84515; CAA59144; 1;
 DR EMBL: X17373; CAA35246; 1;
 DR PIR: S13800; S13800.
 DR MGD: MGI:95301; E113.
 DR InterPro: IPR00717; Spectrin.
 DR InterPro: IPR002017; Spectrin.
 DR Pfam: PF01369; PC1; 1.
 DR SMART: SM00088; PINP; 1.
 DR Initiation factor; Protein biosynthesis; Repeat; Phosphorylation.
 FT DOMAIN 924 ->133 21 X 10 AA TANDEM REPEAT OF D-[DE]-D-R-
 FT CONFLICT 613 647
 FT PROKGKAREKERILOHEQDVKVIVSERIQLKKF->
 FT PRKGKAREGTDNSRANQFNCSAVAEQDFDR (IN
 REF. 2 AND 3).
 FT CONFLICT 683 684 EL -> DY (IN REF. 2 AND 3).
 FT CONFLICT 717 717 Q -> H (IN REF. 2 AND 3).
 FT CONFLICT 766 766 A -> V (IN REF. 2 AND 3).
 FT CONFLICT 787 790 RHSR -> SIVA (IN REF. 3).
 FT CONFLICT 793 793 F -> D (IN REF. 2).
 SQ SEQUENCE 1344 AA; 161949 MW; FQCAE2169F577712 CRC64;

Query Match 6238; Score 43; DB 1; Length 1344;
 Best Local Similarity 50.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 OY 1 EREKEMMREKEEL 14
 Db 618 EREKERILOQUEUQI 631

Search completed: January 16, 2003, 16:51:09
 Job time : 22.4 secs

